

Alignment of SSC nectin1 extra cellular domain(VCC), as defined in sequence 2 and bovine nectin1 extracellular domain (as from gi:XP612918)

Multalin version 5.4.1

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Published research using this software should cite

Multiple sequence alignment with hierarchical clustering

F. CORPET, 1988, Nucl. Acids Res., 16 (22), 10881-10890

Symbol comparison table: blosum62

Gap weight: 12

Gap length weight: 2

Consensus levels: high=90% low=50%

Consensus symbols:

! is anyone of IV

\$ is anyone of LM

% is anyone of FY

is anyone of NDQEBZ

MSF: 336 Check: 0

Name: SSC-ECD(seq.2) Len: 336 Check: 8371 Weight: 1.00

Name: BTA-ECD(gi:XP612918) Len: 336 Check: 8260 Weight: 1.00

Name: Consensus Len: 336 Check: 4256 Weight: 0.00

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1
SSC-ECD(seq.2) MARMGLAGAA GRNWGLALGL TAFFLPGAHT QVVQVNDMSY GFIGTDVVLH
BTA-ECD(gi:XP612918) MARMGLAGAA GRNWGLALGL TAFFLPGAQA QMVQVNDMSY GFIGTDVVLH
Consensus MARMGLAGAA GRNWGLALGL TAFFLPGAga QmVQVNDMSY GFIGTDVVLH

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51
SSC-ECD(seq.2) CSFANPLPGV KITQVTWQKA TNGSKQNVAI YNPAMGVSVL APYRERVEFL
BTA-ECD(gi:XP612918) CSFANPLPGV KITQVTWQKA TNGSKQNVAI YNPAMGVSVL APYRERVEFL
Consensus CSFANPLPGV KITQVTWQKA TNGSKQNVAI YNPAMGVSVL APYRERVEFL

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101
SSC-ECD(seq.2) RPSFTDGTIR LSRLELEDEG VYICEFATFP AGNRESQNLN TVMAKPTNWI
BTA-ECD(gi:XP612918) RPSFTDGTIR LSRLELEDEG VYICEFATFP AGNRESQNLN TVMAKPTNWI
Consensus RPSFTDGTIR LSRLELEDEG VYICEFATFP AGNRESQNLN TVMAKPTNWI

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151
SSC-ECD(seq.2) EGTQAVLRAR KGKDDKVLVA TCTSANGKFP SVVSWETHLK GEAEYQBIIRN
BTA-ECD(gi:XP612918) EGTQAVLRAR KGQDEKVLVA TCTSANGKFP SVVSWETHLK GEAEYQBIIRN
Consensus EGTgAVLRAR KGgD#KVLVA TCTSANGKFP SVVSWETHLK GEAEYQBIIRN

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201
SSC-ECD(seq.2) PNGTVTVISR YRLVPSREDH RQSLACIVNY HMDFRESLT LNVQYEPEVT
BTA-ECD(gi:XP612918) PNGTVTVISR YRLVPSREAH RQSLACIVNY HMDFRESLT LNVQYEPEVT
Consensus PNGTVTVISR YRLVPSREAh RQSLACIVNY HMDFRESLT LNVQYEPEVT

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251
SSC-ECD(seq.2) IEGFDGNWYL QRMDVKLTCK ADANPPATEY HWTTLNGSLP KGVEAQNRNL
BTA-ECD(gi:XP612918) IEGFDGNWYL QRMDVKLTCK ADANPPATEY HWTTLNGSLP KGVEAQNRNL
Consensus IEGFDGNWYL QRMDVKLTCK ADANPPATEY HWTTLNGSLP KGVEAQNRNL

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301 336
SSC-ECD(seq.2) FFRGFINYSM AGTYICEATN PIGTRSGQVE VNITEF
BTA-ECD(gi:XP612918) FFRGFINYSL AGTYVCEATN PIGTRSAQVE VNITEF
Consensus FFRGFINYS$ AGTYICEATN PIGTRSaQVE VNITEF

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13 aa.changes over 336 residues